RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _08/444,791_
Source: _1 FW 16_
Date Processed by STIC: _12/20/04_

ENTERED

RAW SEQUENCE LISTING   DATE: 12/20/2004
PATENT APPLICATION: US/08/444,791   TIME: 13:10:36

Input Set : A:\40451C.txt
Output Set: N:\CRF4\12202004\H444791.raw

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 3 <110> APPLICANT: Brockhaus, et al.
 5 <120> TITLE OF INVENTION: Human TNF Receptor
 7 <130> FILE REFERENCE: 01017/40451C
 9 <140> CURRENT APPLICATION NUMBER: US 08/444,791
10 <141> CURRENT FILING DATE: 1995-05-19
12 <150> PRIOR APPLICATION NUMBER: CH 3319/89
13 <151> PRIOR FILING DATE: 1989-09-12
15 <150> PRIOR APPLICATION NUMBER: CH 786/90
16 <151> PRIOR FILING DATE: 1990-03-08
18 <150> PRIOR APPLICATION NUMBER: CH 1347/90
19 <151> PRIOR FILING DATE: 1990-04-20
21 <150> PRIOR APPLICATION NUMBER: US 07/580,013
22 <151> PRIOR FILING DATE: 1990-09-10
24 <150> PRIOR APPLICATION NUMBER: US 08/095,640
25 <151> PRIOR FILING DATE: 1993-07-21
27 <160> NUMBER OF SEQ ID NOS: 26
29 <170> SOFTWARE: PatentIn version 3.3
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 2111
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
36 <400> SEQUENCE: 1
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39 ccctcaactg tcaccccaag gcacttggga cgtcctggac agaccgagtc ccgggaagcc    120
41 ccagcactgc cgctgccaca ctgccctgag cccaaatggg ggagtgagag gccatagctg    180
43 tctggcatgg gcctctccac cgtgcctgac ctgctgctgc cgctggtgct cctggagctg    240
45 ttggtgggaa tataccctc aggggttatt ggactggtcc ctcacctagg gacagggag    300
47 aagagagata gtgtgtgtcc ccaaggaaaa tatatccacc ctcaaaataa ttcgatttgc    360
49 tgtaccaagt gccacaaagg aacctacttg tacaatgact gtccaggccc ggggcaggat    420
51 acggactgca gggagtgtga gagcggctcc ttcaccgctt cagaaaacca cctcagacac    480
53 tgcctcagct gctccaaatg ccgaaaggaa atgggtcagg tggagatctc ttcttgcaca    540
55 gtggaccggg acaccgtgtg tggctgcagg aagaaccagt accggcatta ttggagtgaa    600
57 aacctttttcc agtgcttcaa ttgcagcctc tgcctcaatg ggaccgtgca cctctcctgc    660
59 caggagaaac agaacaccgt gtgcacctgc catgcaggtt tctttctaag agaaaacgag    720
61 tgtgtctcct gtagtaactg taagaaaagc ctggagtgca cgaagttgtg cctaccccag    780
63 attgagaatg ttaagggcac tgaggactca ggcaccacag tgctgttgcc cctggtcatt    840
65 ttctttggtc tttgcctttt atccctcctc ttcattggtt taatgtatcg ctaccaacgg    900
67 tggaagtcca agctctactc cattgtttgt gggaaatcga cacctgaaaa agagggggag    960
69 cttgaaggaa ctactactaa gcccctggcc ccaaacccaa gcttcagtcc cactccaggc   1020
71 ttcacccccca ccctgggctt cagtcccgtg cccagttcca ccttcacctc cagctccacc   1080
73 tatacccccg gtgactgtcc caactttgcg gctccccgca gagaggtggc accaccctat   1140
75 caggggctg acccccatcct tgcgacagcc ctcgcctccg accccatccc caacccccTt   1200
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 83 gcgcaataca gcatgctggc gacctggagg cggcgcacgc cgcggcgcga ggccacgctg  1440
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 87 gaggcgcttt gcggccccgc cgccctcccg cccgcgccca gtcttctcag atgaggctgc  1560
 89 gcccctgcgg gcagctctaa ggaccgtcct gcgagatcgc cttccaaccc cacttttttc  1620
 91 tggaaaggag gggtcctgca ggggcaagca ggagctagca gccgcctact tggtgctaac  1680
 93 ccctcgatgt acatagcttt tctcagctgc ctgcgcgccg ccgacagtca gcgctgtgcg  1740
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 97 acgctatgcc tcatgcccgt tttgggtgtc ctcaccagca aggctgctcg ggggcccctg  1860
 99 gttcgtccct gagccttttt cacagtgcat aagcagtttt ttttgttttt gttttgtttt  1920
101 gttttgtttt taaatcaatc atgttacact aatagaaact tggcactcct gtgccctctg  1980
103 cctggacaag cacatagcaa gctgaactgt cctaaggcag gggcgagcac ggaacaatgg  2040
105 ggccttcagc tggagctgtg gacttttgta catacactaa aattctgaag ttaaaaaaaa  2100
107 aacccgaatt c                                                        2111
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111 <211> LENGTH: 455
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 2
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122             20                  25                  30
125 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
126         35                  40                  45
129 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
130     50                  55                  60
133 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
134 65                  70                  75                  80
137 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
138             85                  90                  95
141 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
142             100                 105                 110
145 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
146         115                 120                 125
149 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
150     130                 135                 140
153 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
154 145                 150                 155                 160
157 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
158             165                 170                 175
161 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
162             180                 185                 190
165 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
166         195                 200                 205
169 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
170     210                 215                 220
173 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
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177 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
178               245               250               255
181 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
182               260               265               270
185 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
186               275               280               285
189 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
190       290               295               300
193 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
194 305               310               315               320
197 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
198               325               330               335
201 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
202               340               345               350
205 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
206       355               360               365
209 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
210       370               375               380
213 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
214 385               390               395               400
217 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
218               405               410               415
221 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
222               420               425               430
225 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
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229 Pro Ala Pro Ser Leu Leu Arg
230       450               455
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234 <211> LENGTH: 2339
235 <212> TYPE: DNA
236 <213> ORGANISM: Homo sapiens
238 <400> SEQUENCE: 3
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243 actcgggaac agaaccgcat ctgcacctgc aggcccggct ggtactgcgc gctgagcaag   180
245 caggaggggt gccggctgtg cgcgccgctg ccgaagtgcc gcccgggctt cggcgtggcc   240
247 agaccaggaa ctgaaacatc agacgtggtg tgcaagcccct gtgccccggg gacgttctcc   300
249 aacacgactt catccacgga tatttgcagg ccccaccaga tctgtaacgt ggtggccatc   360
251 cctgggaatg caagcaggga tgcagtctgc acgtccacgt cccccacccg gagtatggcc   420
253 ccaggggcag tacacttacc ccagccagtg tccacacgat cccaacacac gcagccaagt   480
255 ccagaaccca gcactgctcc aagcacctcc ttcctgctcc caatgggccc cagcccccca   540
257 gctgaaggga gcactggcga cttcgctctt ccagttggac tgattgtggg tgtgacagcc   600
259 ttgggtctac taataatagg agtggtgaac tgtgtcatca tgacccaggt gaaaaagaag   660
261 cccttgtgcc tgcagagaga agccaaggtg cctcacttgc ctgccgataa ggcccggggt   720
263 acacagggcc ccgagcagca gcacctgctg atcacagcgc cgagctccag cagcagctcc   780
265 ctggagagct cggccagtgc gttggacaga agggcgccca ctcggaacca gccacaggca   840
267 ccaggcgtgg aggccagtgg ggccggggag ccccgggcca gcaccgggag ctcagcagat   900
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269 tcttcccctg gtggccatgg gacccaggtc aatgtcacct gcatcgtgaa cgtctgtagc   960
271 agctctgacc acagctcaca gtgctcctcc caagccagct ccacaatggg agacacagat  1020
273 tccagcccct cggagtcccc gaaggacgag caggtcccct tctccaagga ggaatgtgcc  1080
275 tttcggtcac agctggagac gccagagacc ctgctgggga gcaccgaaga gaagcccctg  1140
277 cccttggag tgcctgatgc tgggatgaag cccagttaac caggccggtg tgggctgtgt  1200
279 cgtagccaag gtggctgagc cctggcagga tgaccctgcg aaggggccct ggtccttcca  1260
281 ggcccccacc actaggactc tgaggctctt tctgggccaa gttcctctag tgccctccac  1320
283 agccgcagcc tccctctgac ctgcaggcca agagcagagg cagcgagttg tggaaagcct  1380
285 ctgctgccat ggcgtgtccc tctcggaagg ctggctgggc atggacgttc ggggcatgct  1440
287 ggggcaagtc cctgagtctc tgtgacctgc cccgcccagc tgcacctgcc agcctggctt  1500
289 ctggagccct tgggtttttt gtttgtttgt ttgtttgttt gtttgtttct cccctgggc  1560
291 tctgcccagc tctggcttcc agaaaacccc agcatccttt tctgcagagg ggctttctgg  1620
293 agaggaggga tgctgcctga gtcacccatg aagacaggac agtgcttcag cctgaggctg  1680
295 agactgcggg atggtcctgg ggctctgtgc agggaggagg tggcagccct gtaggaacg  1740
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299 tcacgcctat gatcccagca ctttgggagg ctgaggcggg tggatcacct gaggttagga  1860
301 gttcgagacc agcctggcca acatggtaaa accccatctc tactaaaaat acagaaatta  1920
303 gccgggcgtg gtggcgggca cctatagtcc cagctactca gaagcctgag gctgggaaat  1980
305 cgtttgaacc cgggaagcgg aggttgcagg gagccgagat cacgccactg cactccagcc  2040
307 tgggcgacag agcgagagtc tgtctcaaaa gaaaaaaaaa aagcaccgcc tccaaatgct  2100
309 aacttgtcct tttgtaccat ggtgtgaaag tcagatgccc agagggccca ggcaggccac  2160
311 catattcagt gctgtggcct gggcaagata acgcacttct aactagaaat ctgccaattt  2220
313 tttaaaaaag taagtaccac tcaggccaac aagccaacga caaagccaaa ctctgccagc  2280
315 cacatccaac cccccacctg ccatttgcac cctccgcctt cactccggtg tgcctgcag  2339
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321 <211> LENGTH: 392
322 <212> TYPE: PRT
323 <213> ORGANISM: Homo sapiens
325 <400> SEQUENCE: 4
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331 Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
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335 Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
336          35                  40                  45
339 Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
340      50                  55                  60
343 Arg Leu Cys Ala Pro Leu Pro Lys Cys Arg Pro Gly Phe Gly Val Ala
344 65                  70                  75                  80
347 Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
348              85                  90                  95
351 Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
352              100                 105                 110
355 Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala
356          115                 120                 125
359 Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
360      130                 135                 140
363 His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Ser
364 145                 150                 155                 160
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367 Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
368   165   170   175
371 Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val
372   180   185   190
375 Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val
376   195   200   205
379 Val Asn Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu
380   210   215   220
383 Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly
384 225   230   235   240
387 Thr Gln Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser
388   245   250   255
391 Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala
392   260   265   270
395 Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala
396   275   280   285
399 Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Ala Asp Ser Ser Pro Gly
400   290   295   300
403 Gly His Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser
404 305   310   315   320
407 Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met
408   325   330   335
411 Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val
412   340   345   350
415 Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro
416   355   360   365
419 Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val
420   370   375   380
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424 385   390
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428 <211> LENGTH: 28
429 <212> TYPE: PRT
430 <213> ORGANISM: Artificial sequence
432 <220> FEATURE:
433 <223> OTHER INFORMATION: Synthetic peptide
435 <220> FEATURE:
436 <221> NAME/KEY: misc_feature
437 <222> LOCATION: (25)..(25)
438 <223> OTHER INFORMATION: Xaa = any or unknown amino acid
440 <400> SEQUENCE: 5
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443 1   5   10   15
W--> 446 Gln Gly Lys Tyr Ile His Pro Glu Xaa Asn Ser Ile
447   20   25
449 <210> SEQ ID NO: 6
450 <211> LENGTH: 15
451 <212> TYPE: PRT
452 <213> ORGANISM: Artificial sequence

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/20/2004
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Input Set : A:\40451C.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 25
Seq#:10; Xaa Pos. 8
Seq#:11; Xaa Pos. 2
Seq#:14; Xaa Pos. 9,10,13

VERIFICATION SUMMARY   DATE: 12/20/2004
PATENT APPLICATION: **US/08/444,791**   TIME: 13:10:37

Input Set : **A:\40451C.txt**
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L:526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:601 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
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